AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 1, at line 1 as follows:

<u>METHODS FOR</u> MICROBIAL IDENTIFICATION CHIP BASED ON DNA-DNA HYBRIDIZATION

Please replace the paragraph beginning on page 32, at line 5 as follows:

In this Example, the production of one microarray embodiment is described. Genomic DNAs from four fluorescent *Pseudomonas* strains (*Pseudomonas fluorescens* (ATCC 13525^T), *P. chlororaphis* (ATCC 9447), *P. putida* (ATCC 12633^T), and *P. aeruginosa* (ATCC 15692); *i.e.*, the "reference strains") were fragmented by bead-beating to ensure randomness, and the fragments were size-fractionated (1 to 2 kb) by agarose gel electrophoresis, as known in the art. The QIAquiek QIAQUICK Gel Extraction Kit (Qiagen) was used to elute and purify DNA from the agarose gel, according to the manufacturer's instructions. The genomic DNA fragments were inserted to pPCR-Script Amp vector (Stratagene), then PCR amplified with the T3/T7 promoter primer set using standard PCR conditions, with a primer annealing temperature of 55°C. Amplified genomic DNA fragments were purified with QIAquiek QIAQUICK 8 PCR purification kit (Qiagen) and quantified with PieoGreen PICOGREEN (Molecular Probes), according to the manufacturer's instructions.

Please replace the paragraph beginning on page 32, at line 18 as follows:

Purified DNAs were resuspended (200 ng/µl) in 3X SSC (1X SSC is 0.15 M NaCl, plus 0.015 M sodium citrate), and printed using approximately 1 nl/spot, on CMT-GAPS amino silane coated slides (Corning). In these experiments, 92, 90, 96, and 60 fragments from *P. fluorescens, P. chlororaphis, P. putida*, and *P. aeruginosa* were spotted in duplicate, respectively. Yeast gene *STE* (pheromone receptor gene; GenBank GENBANK accession no. M12239) was spotted as positive control, and yeast gene *ACT* (actin gene; GenBank GENBANK accession no. L00026), lambda DNA, and water were spotted as negative controls. PCR primer pair, STE3F1 (CCC CTT CAA AAT TGG AGC TTG C; SEQ ID NO:1) and STE3R1 (CCC CCT TTA GCA TGG CAT TCA; SEQ ID NO:2), and pair ACT1F1 (GAT GGA GCC AAA GCG GTG A (SEQ ID NO:3) and ACT1R1 (GCG CTT

GCA CCA TCC CAT T; SEQ ID NO:4) were used to amplify the STE and ACT yeast genes, respectively.

Please replace the paragraph beginning on page 33, at line 25 as follows:

In this Example, the methods used to analyze the data obtained from the hybridized arrays of one embodiment of the present invention are described. Hybridized arrays were scanned with a GenePix GENEPIX 4000 laser scanner (Axon). Laser lights of wavelength at 532 and 635 nm were used to excite Cy3 dye and Cy5 dyes, respectively. Fluorescent images were captured as multi-image-tagged image file format (TIFF) and analyzed with GenePix GENEPIX Pro 3.0 software (Axon). The ratio (R) of the extent of hybridization between test DNAs and reference DNAs was derived from a median value of pixel-by-pixel ratios. By using this approach to calculate R, non-specific signals, which appear in both wavelength images, were found to have less of an effect than when the mean values of a whole spot were used.

Please replace the paragraph beginning on page 36, at line 7 as follows:

In addition, situations in which different strains of the same species have differences in genome size (e.g., E. coli K12, as compared to E. coli O157; GenBank GENBANK accession nos. U00096 and AE005174, respectively) were taken into consideration. It is not contemplated that this scale of difference (1 of 5 Mb) will invalidate the methods of the present invention, although the percent similarity should be slightly higher than the average percent similarity from whole-genome DNA-DNA hybridization.